Cationic State Distribution over the P700 Chlorophyll Pair in Photosystem I

Keisuke Saito[†] and Hiroshi Ishikita[†‡*]

[†]Career-Path Promotion Unit for Young Life Scientists, Graduate School of Medicine, Kyoto University, Kyoto, Japan; and [‡]Japan Science and Technology Agency, PRESTO, Saitama, Japan

ABSTRACT The primary electron donor P700 in photosystem I is composed of two chlorophylls, P_A and P_B. P700 forms the cationic $[P_A/P_B]^{\bullet+}$ state as a result of light-induced electron transfer. We obtained a $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 28:72 and a spin distribution of 22:78 for the entire PSI protein-pigment complex. By considering the influence of the protein components on the redox potential for one-electron oxidation of P_A/P_B monomers, we found that the following three factors significantly contributed to a large $P_B^{\bullet+}$ population relative to $P_A^{\bullet+}$: 1), Thr-A743 forming a H-bond with P_A; 2), P_A as a chlorophyll *a* epimer; and 3), a conserved PsaA/PsaB pair, the Arg-A750/Ser-B734 residue. In addition, 4), the methyl-ester groups of the accessory chlorophylls A_{-1A}/A_{-1B} significantly stabilized the cationic $[P_A/P_B]^{\bullet+}$ state and 5), the methyl-ester group orientations were completely different in A_{-1A} and A_{-1B} as seen in the crystal structure. When the methyl-ester group was rotated, the spin-density distribution over P_A/P_B ranged from 22:78 to 15:85.

INTRODUCTION

In oxygenic photosynthesis, photosystem I (PSI) participates in the conversion of light to chemical energy with photosystem II (PSII). Light-induced electron transfer occurs along a series of cofactors bound to the PsaA and PsaB subunits of PSI. On the lumen side, there exists a chlorophyll dimer P700 composed of two chlorophylls P_A and P_B. P_B is chlorophyll *a* (Chl*a*) and P_A is Chl*a*′, the $C13^2$ epimer of Chl*a* (Fig. 1 *a*) (1,2). A second Chl*a* pair next to P_A/P_B is the accessory Chl*a* A_{-1A}/A_{-1B}. In addition, there are two additional distant Chl*a* (A_0), two phylloquinones (A_1), and one iron-sulfur cluster (F_X) in the PsaA/PsaB subunits. Similar to PSII, these six Chl*a* and two phylloquinones are arranged in two electron-transfer branches (A and B), which adopt a pseudo-C_2 symmetry with the rotation axis passing through P_A/P_B and F_X. In PSII, only one of the two branches serves as an electron-transfer active branch; this is in contrast to PSI, in which two branches are electron-transfer active (3), as shown by the biphasic forward electron transfers from P700 to A_1 or from A_1 to F_X observed in kinetic studies.

The primary process of charge separation culminates with a hole on the P_A/P_B pair in PSI or on the P_{D1}/P_{D2} pair in PSII. In PSII, the cationic state over P_{D1}/P_{D2} is predominantly observed in the Chl*a* of the electron active branch P_{D1}, with a $P_{D1}^{\bullet+}/P_{D2}^{\bullet+}$ ratio of ~80:20 (4,5). For PSI, the $P_A^{\bullet+}/P_B^{\bullet+}$ ratios or the corresponding spin-density distributions were obtained experimentally by Fourier transform infrared (FTIR) spectroscopy (6) or electron paramagnetic resonance (EPR) (4,7,8) studies, respectively. FTIR studies indicated that the $P_A^{\bullet+}/P_B^{\bullet+}$ ratios were in the range of 50:50–33:67 (6). On the other hand, the spin-density distribution over P_A/P_B is 25:75 (4) and 25:75–20:80 in PSI from spinach (7) and 15:85 in PSI from *Thermosynechococcus elongatus* (8) (reviewed in Webber and Lubitz (9)).

To understand the role of the amino-acid residues or cofactors of PSI in the energetics of P700, influences of all amino-acid residues and redox-active cofactors on the energetics of P_A/P_B Chl*a* monomers as well as the P700 Chl*a* dimer are, for the first time to our knowledge, here elucidated. We present the following: 1), The computational results of the influence of the PSI protein environment on the redox potentials, $E_m(P_A)$ and $E_m(P_B)$, are presented on the basis of the PSI crystal structure (2) in the presence of all protein subunits and cofactors. The linear Poisson-Boltzmann equation is solved by considering the protonation states of all titratable sites in PSI. 2), The $P_A^{\bullet+}/P_B^{\bullet+}$ ratio for the P_A/P_B pair is calculated using a large-scale quantum chemical/molecular mechanical (QM/MM) approach with explicit treatment of the complete PSI atomic coordinates divided into two subsystems; the QM region contains the P_A/P_B dimer and is treated by quantum mechanics (unrestricted DFT/B3LYP and LACVP* level) and the remaining protein subunits and cofactors are treated with the MM force field. The computational conditions and procedures used in studies on the *Thermosynechococcus vulcanus* PSII (10) (using the 1.9 Å structure (11)) were consistently used in our study. This can facilitate the direct analysis and comparison of the influences of protein environments on Chl*a* in both PSI and PSII.

EXPERIMENTAL PROCEDURES

In this article, we employed the following systematic modeling procedure:

First, we constructed a realistic molecular model of the whole PSI protein-pigment complex using a high-resolution crystal structure. Based on this atomistic model, we evaluated the redox potential of P_A/P_B by

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*Correspondence: hiro@cp.kyoto-u.ac.jp

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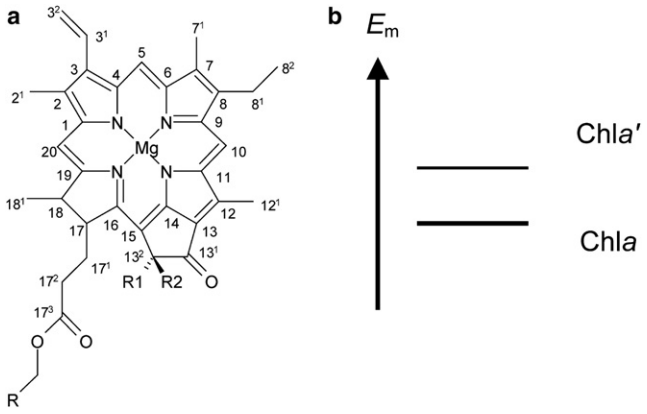

FIGURE 1 (*a*) Geometry of Chl*a* (R1 = CH_3COO-, R2 = H) and the $C13^2$ epimer, Chl*a*′ (R1 = H, R2 = CH_3COO-). (*b*) E_m values of Chl*a* and Chl*a*′ in the reference system (e.g., aprotic solvents).

solving the linear Poisson-Boltzmann equation with explicit consideration of the protonation states for all titratable residues.

Second, to gain deeper insights into the electronic structure of P_A/P_B Chl*a*′/Chl*a* heterodimer, we performed large-scale QM/MM calculations for the entire PSI protein-pigment complex.

Third, and finally, after confirming the validity of the computational results through comparison with available experimental data, we discussed the atomistic origin that determines the asymmetric distribution of the cationic state of the P_A/P_B pair. Technical details of each modeling procedure are summarized as follows.

Coordinates

The atomic coordinates were taken from the x-ray structure of the PSI protein-pigment complex from *T. elongatus* at 2.5 Å resolution (Protein Data Bank code: 1JB0) (11). Hydrogen atoms were generated and energetically optimized using the CHARMM force field (12). The positions of all nonhydrogen atoms were fixed, and all titratable groups were kept in their standard protonation states; i.e., acidic groups were ionized and basic groups were protonated. For the QM/MM calculations, we added additional counterions to neutralize the whole system.

Atomic partial charges

Atomic partial charges of the amino acids were adopted from the all-atom CHARMM22 (13) parameter set. The charges of the protonated acidic O atoms were increased successively by +0.5 units to implicitly account for the presence of a proton. Similarly, instead of removing a proton to generate the deprotonated state, the charges of all of the protons of the basic groups of Arg and Lys were successively diminished to a total of 1 unit of charge. For residues for which the protonation states were not available in the CHARMM22 parameter set, appropriate charges were computed (14). For the atomic charges of Chl*a* (except for P_A/P_B) and quinones, we used atomic partial charges from previous studies on PSI (15–17); the charges were determined by fitting the surrounding electrostatic potential of these molecules using the RESP procedure (18). The charges of equivalent H atoms (e.g., three H atoms of methyl group) were averaged. The electronic wave functions were calculated after geometry optimization with the DFT module in JAGUAR (19) (B3LYP/LACVP*) (see Table S1 in the Supporting Material).

Computation of redox potential E_m(Chl*a*)

Our computation was based on the electrostatic continuum model, where the linear Poisson-Boltzmann equation was solved using the MEAD program (20). To facilitate direct comparisons with previous computational results, identical computational conditions and parameters such as atomic partial charges and dielectric constants were used (21,22). The redox states of all other cofactors (e.g., A_{-1} and A_0 Chl*a*, and A_1 quinone) were kept in their neutral charge states during the redox titration of each Chl*a*. We considered F_X, F_A, and F_B in the oxidized charge state $[Fe_4S_4(SCH_3)_4]^{2-}$ for the wild-type PSI as in previous studies (15–17). The ensemble of the protonation patterns was sampled using the Monte Carlo method with the Karlsberg program (http://agknapp.chemie.fu-berlin.de/karlsberg/(1999)) (23). The dielectric constants were set to $\varepsilon_p = 4$ inside the protein and $\varepsilon_w = 80$ for water.

All computations were performed at 300 K, pH 7.0, and an ionic strength of 100 mM. The linear Poisson-Boltzmann equation was solved using a three-step grid-focusing procedure at resolutions of 2.5, 1.0, and 0.3 Å. The Monte Carlo sampling for a redox-active group yielded the probabilities $[A_{ox}]$ and $[A_{red}]$ of the two redox states of molecule A. The shifts in E_m(Chl*a*′) and E_m(Chl*a*) due to the PSI protein environment were evaluated using the Nernst equation. A bias potential was applied to obtain an equal amount of both redox states ($[A_{ox}] = [A_{red}]$), yielding the redox midpoint potential E_m as the resulting bias potential. For convenience, the computed E_m was represented in millivolt accuracy and the last digit was not considered to be significant.

QM/MM calculations

In all QM/MM calculations reported here, we employed the so-called electrostatic embedding QM/MM scheme. In all the QM/MM calculations, we used the QSITE (24) program code. The electrostatic and steric effects created because of the complex PSI architecture were explicitly considered in all calculations. Owing to the large system size of PSI, the QM region was limited to the P_A/P_B Chl*a*′/Chl*a* heterodimer for simplicity, whereas the other protein units and all cofactors were approximated by the MM force field. Because the atomic partial charges were optimized (e.g., A_{-1} and A_0 Chl*a*, and A_1 quinone), the QM/MM partition was accurate enough to describe the electronic structure of the $[P_A/P_B]^{\bullet+}$ Chl*a*′/Chl*a* heterodimer. To reliably determine the cationic character of the $[P_A/P_B]^{\bullet+}$ heterodimer, we employed the unrestricted DFT method with the B3LYP functional and LACVP* basis sets. The $[P_A/P_B]^{\bullet+}$ heterodimer geometry was refined by the constrained QM/MM optimizations; for the surrounding MM protein environment, the atomistic coordinates were exactly fixed with the original x-ray coordinates. After obtaining the stable geometry of the QM fragment, we determined the ESP charges for the cationic state of the $[P_A/P_B]^{\bullet+}$ heterodimer in the presence of the entire group of PSI atomic coordinates (see Table S1).

RESULTS AND DISCUSSION

$P_A^{\bullet+}/P_B^{\bullet+}$ ratio and spin-density distribution in wild-type PSI

The $P_A^{\bullet+}/P_B^{\bullet+}$ ratio was calculated to be 27.9:72.1 (Table 1), demonstrating that the cationic state is stabilized more in P_B than in P_A: this should result in the value of $E_m(P_B)$ being lower than that of $E_m(P_A)$. The $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 27.9:72.1 was considerably close to the charge-distribution ratio of 33:67 obtained from FTIR studies of PSI from *Synechocystis* sp. PCC 6803 (6). The calculated spin-density distribution over P_A/P_B was 22.4:77.6 (Table 1), which shows greater asymmetry than the ratio of the charge distribution (i.e., $P_A^{\bullet+}/P_B^{\bullet+}$), a fact already pointed out previously in PSII (25,26). The obtained value was in good agreement with the experimental values of 25:75 (4) and

TABLE 1 Values of $E_m(P_A)$, $E_m(P_B)$ (in mV), $P_A^{\bullet+}/P_B^{\bullet+}$ ratios, and spin-density distributions in the PSI protein (in %)

(Factor)		E_m shift (versus reference)		Charge		Spin	
		P_A	P_B	$P_A^{\bullet+}$	$P_B^{\bullet+}$	P_A	P_B
	Wild-type	29*	27	27.9	72.1	22.4	77.6
(1)	T743V [H-bond]	20*	28	32.2	67.8	26.9	73.1
(2)	CH_3COO- deleted [Epimer]			32.2	67.8	29.7	70.3
(3)	Δ(Arg-A750/Ser-B734) [PsaA/PsaB pair]			30.6	69.4	25.0	75.0
(4)	$\Delta(A_{-1A}/A_{-1B})$ [Cofactor]			24.0	76.0	18.7	81.3

The symbol Δ stands for deletion of atomic charges of the residues/groups.
*Because E_m(Chla') in the reference model system is unknown, only the E_m shift was calculated. An actual E_m(Chla') may be higher than E_m(Chl$a$) because Chla' is thermodynamically less stable than Chl$a$ (9).

25:75–20:80 of PSI from spinach (7) and 15:85 of PSI from *T. elongatus* (8) (note: according to another interpretation of the *T. elongatus* data (8), the ratio of 25:75–30:70 may be possible (9)).

The PSI protein environment shifted the E_m values of P_A/P_B only marginally from those of the reference model system (Table 1). The shifts were essentially the same for P_A and P_B. However, the resulting E_m values for the P_A/P_B molecules must be different because of the difference between E_m(Chla') and E_m(Chl$a$) in the reference model system. Although the difference between E_m(Chla') and E_m(Chl$a$) is not known so far, we infer that the former may be higher than the latter because Chla' is thermodynamically less stable than Chl$a$ (Fig. 1 *b*) (9).

Influence of H-bond on the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio

The −OH group of Thr-A743 can form an H-bond with the 13^1-keto group of P_A, whereas the corresponding H-bond is absent in P_B. A mutation of Thr-A743 to Val would result in the loss of the H-bond (27,28). Using the wild-type PSI crystal structure, we modeled the T(A743)V PSI by substituting the −OH side chain group of Thr with $–CH_3$ (followed by geometry optimization of the A743 side chain whereas all of the other parts remained fixed).

$E_m(P_A)$ was lowered by ~10 mV upon the T(A743)V mutation whereas $E_m(P_B)$ remained unchanged (Table 1). The marginal downshift in $E_m(P_A)$ was in agreement with a relatively weak H-bond of Thr-A743, as pointed out in spectroscopic studies (29). As $E_m(P_A)$ was lowered (i.e., $P_A^{\bullet+}$ was stabilized), the calculated $P_A^{\bullet+}/P_B^{\bullet+}$ ratio was significantly shifted and the population of $P_A^{\bullet+}$ increased from 27.9 in the wild-type PSI to 32.2 in the T(A743)V PSI (Table 1). This observed $P_A^{\bullet+}$ population shift is in agreement with 1), the previous proposal that deletion of the H-bond leads to a downshift in $E_m(P_A)$ (27), and 2), the experimentally observed relocation of ~14–18% of the cationic state from P_B to P_A upon T(A743)V mutation in PSI from *Chlamydomonas reinhardtii* (28). The slightly smaller relocation of the cationic state (i.e., an increase in $P_A^{\bullet+}$ by 5%) in our study is possibly due to 1), the difference between the used T(A743)V PSI model structure where the −OH group of Thr was replaced with $–CH_3$, without altering the other parts of the atomic coordinates (to avoid an uncertainty of prediction of the protein structure), or 2), the difference of the PSI proteins between *T. elongatus* PSI (corresponds to the crystal structure (2)) and the *Chlamydomonas reinhardtii* PSI. As E_m(P700) differs by up to ~70 mV among different species (30), the P_A/P_B moiety may be slightly different among different species.

The individual values of $E_m(P_A)$ and $E_m(P_B)$ are not known experimentally due to the presence of their coupling. It is particularly difficult to determine $E_m(P_A)$ because of the small amount of $P_A^{\bullet+}$ compared with $P_B^{\bullet+}$. Our study demonstrates that shifts in $E_m(P_A)$ alter the distribution of the cationic (spin) state over P_A/P_B as reported in mutational studies (27,28).

Influence of $C13^2$ epimer Chla' on $P_A^{\bullet+}/P_B^{\bullet+}$ ratio

The asymmetric charge distribution over P_A/P_B may also result from the asymmetry of the molecular geometry in P_A/P_B. The methyl-ester (CH_3COO-) groups in Chla' and Chl$a$ are oppositely orientated with respect to the chlorin plane. Except for this methyl-ester orientation difference, the molecular structures of P_A and P_B are essentially identical (2).

To investigate this orientation difference on the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio, it would have been more relevant to replace Chla' of P_A with Chl$a$. Unfortunately, a replacement of Chla' of P_A with Chl$a$ leads to unreasonable contacts with Tyr-A603, Gly-A739, Thr-A742, and Thr-A743. As an alternative, we substituted the CH_3COO- groups with H in both P_A and P_B (deletion of CH_3COO-), and calculated the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio. Upon deletion of the CH_3COO- groups the $P_A^{\bullet+}$ population increases by ~5% relative to the wild-type PSI, resulting in a $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 32.2:67.8 (Table 1). Thus, the orientation difference in Chla'/Chl$a$ significantly influences the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio in the PSI protein environment.

Under vacuum conditions, the P_A/P_B heterodimer yielded a $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 41.5:58.5 (Table 2), which indicates a considerably delocalized cationic state distribution over P_A/P_B in the absence of the PSI protein environment. The

TABLE 2 Values of $P_A^{\bullet+}/P_B^{\bullet+}$ ratios and spin-density distributions in vacuum (in %)

	Charge		Spin	
	$P_A^{\bullet+}$	$P_B^{\bullet+}$	P_A	P_B
Wild-type	41.5	58.5	38.1	61.9
CH_3COO- deleted	45.5	54.5	46.2	53.8

deletion of CH_3COO- from P_A/P_B delocalized the cationic state, giving a $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 45.5:54.5 (Table 2); i.e., the cationic state is almost equally distributed over P_A/P_B. It can be concluded that in the absence of the PSI protein environment, the orientation of the CH_3COO- group in P_A is predominantly responsible for the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio (Table 3).

Influence of PsaA/PsaB symmetrical residue pairs on the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio

The protein environment, in particular the charged residues, contribute to E_m shifts of the redox active site significantly. Because the E_m difference $E_m(P_A) - E_m(P_B)$ (= ΔE_m) is a key factor that can alter the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio (27) (Fig. 2), it is important to clarify the contributions of residues, in particular those located in the PsaA/PsaB heterodimer subunits.

Arg-A750, located on the lumenal side (Fig. 3 *a*), upshifted $E_m(P_A)$ the most by 65 mV, due to its positively charged protonated state (Table 4). The Arg-A651 on the lumen side and Arg-A728 near F_X, both upshifted $E_m(P_A)$ by 35 mV. Arg-A728 is ~20 Å away from P_A/P_B, but its electrostatic influence on $E_m(P_A)$ and $E_m(P_B)$ is significant because of the complete absence of other titratable residues in the region between P_A/P_B and F_X (Fig. 3 *d*).

As both Arg-A651 and Arg-A728 concomitantly increase $E_m(P_A)$ and $E_m(P_B)$ with almost the same magnitude (Table 4), these residues were not responsible for the asymmetric distribution of $P_A^{\bullet+}/P_B^{\bullet+}$. Furthermore, according to the protein sequence alignment (with the CLUSTAL program (31)), Arg-A651 and Arg-A728 in PsaA are conserved as Arg-B627 and Arg-B712 in PsaB, respectively, which also upshifts $E_m(P_A)$ and $E_m(P_B)$ (Table 4).

TABLE 3 Analysis of factors (listed in Table 1) that differentiate the populations of $P_A^{\bullet+}$ and $P_B^{\bullet+}$ in the PSI protein environment (in %)

	Charge		Spin	
	$P_A^{\bullet+}$	$P_B^{\bullet+}$	P_A	P_B
Wild-type	27.9	72.1	22.4	77.6
(1) + (2)	37.0	63.0	35.1	64.9
(1) + (3)	35.6	64.4	30.5	69.5
(1) + (2) + (3)	40.5	59.5	39.1	60.9

Factors (1) T743V (deletion of a H-bond with PA), (2) CH3COO− substitution with –H (deletion of the Chla′/Chla difference), and (3) deletion of charges of PsaA/PsaB residue pairs responsible for the $E_m(P_A)/E_m(P_B)$ difference.

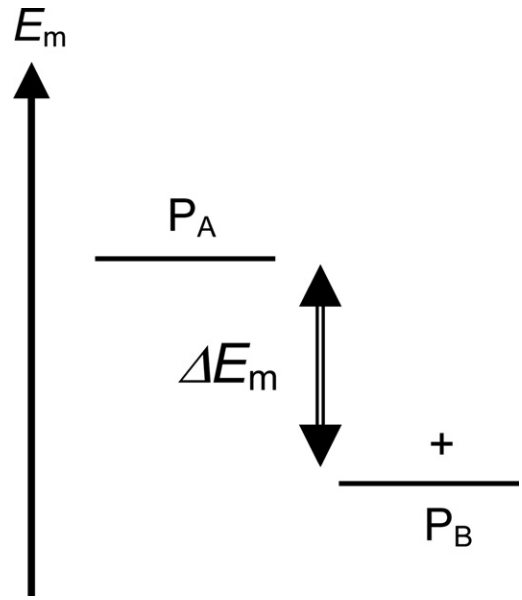

FIGURE 2 Relationship between E_m and population of the cationic state over the P_A/P_B pair. The + sign indicates a population of the energetically distributed cationic state owing to the E_m levels. $\Delta E_m = E_m(P_A) - E_m(P_B)$.

The same argument also holds true for the E_m downshifting residues, which are mainly acidic residues (Table 5). Asp-B444 significantly downshifted $E_m(P_A)$ by 90 mV and $E_m(P_B)$ by 63 mV; and its counterpart in PsaA, Asp-A463, downshifted $E_m(P_A)$ by 67 mV and $E_m(P_B)$ by 98 mV. Thus, the influence of Asp-B444 on ΔE_m is completely compensated for by the influence of the counterpart Asp-A463.

To clarify how the PSI protein environment differentiates $P_A^{\bullet+}/P_B^{\bullet+}$, it is not sufficient to search for the residue that induces large changes in E_m values, instead it is important to find a residue pair of PsaA/PsaB that increases ΔE_m (Fig. 2). Bearing this in mind, we found only a few residue pairs that contribute to nonzero values of ΔE_m. The residue pair, Arg-A750/Ser-B734, increased ΔE_m by 17 mV (Table 6). Note that the residue pair is fully conserved in cyanobacteria and green plants (Fig. 4). The Arg-A750/Ser-B734 pair is located near P_A/P_B on the lumen side (Fig. 3 *c*). Indeed, Arg-A750 was already mentioned as the residue that upshifted $E_m(P_A)$ the most among all residues in PSI (Tables 4 and 5) whereas its counterpart is an uncharged residue, Ser.

In the absence of the atomic charges of Arg-A750/Ser-B734, we obtained the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of 30.6:69.4; in which the $P_A^{\bullet+}$ population has increased by ~3%, with respect to wild-type PSI (Table 1). This result indicates that, in turn, the Arg-A750/Ser-B734 pair contributes to increase the $P_B^{\bullet+}$ population in the wild-type PSI by increasing ΔE_m.

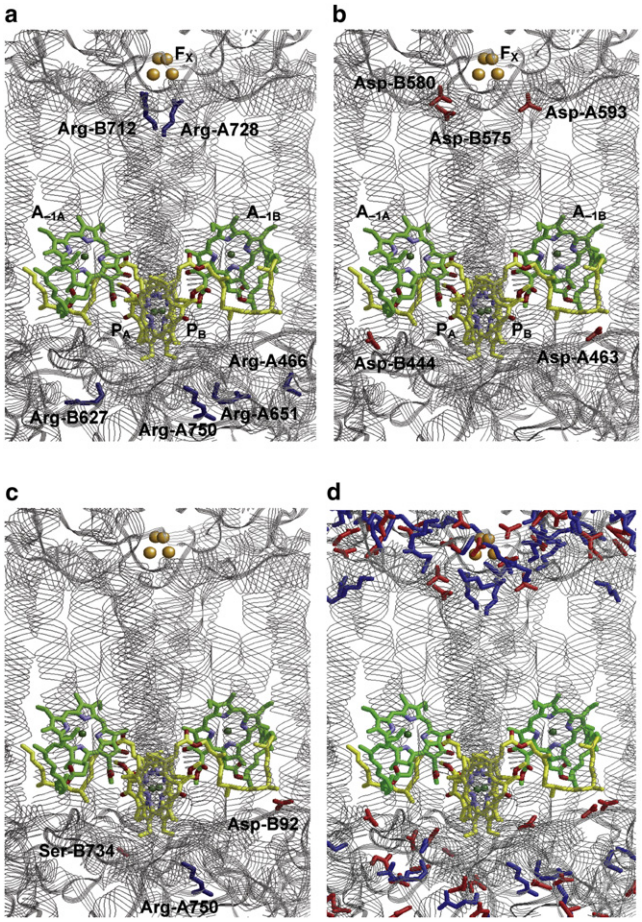

FIGURE 3 Arrangement of residues in PsaA/PsaB of PSI. (*Blue* and *red sticks*) Side chains of basic and acidic residues, respectively. (*a*) Residues increasing $E_m(P_A)$ or $E_m(P_B)$. (*b*) Residues decreasing $E_m(P_A)$ or $E_m(P_B)$. (*c*) Residue pairs enhancing $E_m(P_A) > E_m(P_B)$. (*d*) All acidic and basic residues in PsaA/PsaB.

The Arg-A750/Ser-B734 residue pair contributes the most to ΔE_m among all PsaA/PsaB residue pairs; however, it increases ΔE_m only by 17 mV (Table 6). The second most contributing residue pair —/Asp-B92, in which the corresponding residue in PsaA is absent among cyanobacteria and green plants (Fig. 4), contributes 9 mV to ΔE_m (Table 6). Hence, in comparison with the much larger influence of a number of D1/D2 residue pairs on the $E_m(P_{D1})/E_m(P_{D2})$ difference in PSII (10), the protein environments of PsaA and PsaB in PSI are quite similar in their electrostatic characters.

TABLE 4 Residues that shift $E_m(P_A)$ and $E_m(P_B)$ in the PSI protein environment (mV)

	$E_m(P_A)$ shift				$E_m(P_B)$ shift		
Residue	Side chain	Backbone	Total	Residue	Side chain	Backbone	Total
Increasing $E_m(P_A)$ and $E_m(P_B)$							
Arg-A750	53	12	65	Arg-A651	60	−5	55
Arg-A651	42	−7	35	Arg-A750	30	5	36
Arg-A728	39	−4	35	Arg-A466	32	4	35
Arg-B627	36	−3	33	Arg-B712	36	−4	32
Arg-B712	34	−3	31	Arg-A728	35	−2	32

TABLE 5 Residues that shift $E_m(P_A)$ and $E_m(P_B)$ in the PSI protein environment (mV)

	$E_m(P_A)$ shift				$E_m(P_B)$ shift		
Residue	Side chain	Backbone	Total	Residue	Side chain	Backbone	Total
Decreasing $E_m(P_A)$ and $E_m(P_B)$							
Asp-B444	−94	4	−90	Asp-A463	−102	4	−98
Asp-A463	−70	3	−67	His-B660	−70	6	−64
His-A680	−72	5	−67	Asp-B444	−66	3	−63
A_{-1A}			−65	F_X			−47
F_X			−48	Asp-B575	−42	0	−42
Asp-B575	−41	0	−42	A_{-1B}			−41
Asp-A593	−33	−2	−35	Asp-B580	−31	−2	−33
His-B660	−31	0	−31	His-A680	−31	−1	−32
Asp-B580	−28	−2	−30	Asp-A593	−29	−2	−31

The residue pairs Arg-A750/Ser-B734 and —/Asp-B92 are responsible for ΔE_m in wild-type PSI. Mutations of these residues would produce other protonation patterns of the titratable residues of PSI to compensate for the induced changes (e.g., charges or protein conformations). Unless the protonation pattern of the titratable residues and the protein conformation remain unchanged upon the corresponding mutations, mutational studies do not directly correspond to our results of the wild-type PSI.

Differences in the two accessory Chl*a* pairs A_{-1A} and A_{-1B}

There are also pairs that contribute to decrease ΔE_m and facilitate an accumulation of $P_B^{\bullet+}$. Unexpectedly, the most influential was the accessory Chl*a* pair, A_{-1A} and A_{-1B}, which decreased ΔE_m by 28 mV (Table 7). It was surprising, because both A_{-1A} and A_{-1B} are identical molecules, Chl*a*, and the methyl-ester groups of P_A/P_B, i.e., the region causing the Chl*a*′/Chl*a* difference, is sufficiently far from the interface between P_A/P_B and A_{-1A}/A_{-1B}.

As expected from the ΔE_m value, eliminating the atomic charges of A_{-1A} and A_{-1B} resulted in the decrease in the

TABLE 6 PsaA/PsaB residue pairs responsible for ΔE_m (= $E_m(P_A) - E_m(P_B)$, see Fig. 2) (mV)

PsaA			PsaB			
Residue	$E_m(P_A)$	$E_m(P_B)$	Residue	$E_m(P_A)$	$E_m(P_B)$	ΔE_m
ΔE_m increasing pairs (i.e., pairs that contribute to accumulation of $P_B^{\bullet+}$)						
Arg-A750	65	36	Ser-B734	9	21	17
—	—	—	Asp-B92	−15	−24	9

Contribution to ΔE_m was obtained as [influence of PsaA on $E_m(P_A)$] + [influence of PsaB on $E_m(P_A)$] – [influence of PsaA on $E_m(P_B)$] – [influence of PsaB on $E_m(P_B)$]. PsaA/PsaB residue pairs in each line were generated from the protein sequence alignment performed with the CLUSTAL program (31) (Fig. 4).

```
                    98         108        118         127        137
PsaA T.elongatus    SNYEAWLADP TGIKPSAQVV W-PIVGQGIL NGDVGGGFHG -IQIT-SGLF
PsaA S.6803         SNYEGWLADP THIKPSAQVV W-PIVGQGIL NGDVGGGFHG -IQIT-SGLF
PsaA C.reinhardtii  SNYEAWLSDP THIKPSAQVV W-PIVGQEIL NGDVGGGFQG -IQIT-SGFF
PsaA spinach        SNYEAWLSDP THIGPSAQVV W-PIVGQEIL NGDVGGGFRG -IQIT-SGFF
                    71         81         91          101        111
PsaB T.elongatus    GNFEQWVQDP VNTRPIAHAI WDPQFGKAAV DAFTQAGASN PVDIAYSGVY
PsaB S.6803         GNFEQWIKDP LNIRPIAHAI WDPHFGEGAV NAFTQAGASN PVNIAYSGVY
PsaB C.reinhardtii  GNFEQWVTDP VHIRPIAHAI WDPHFGQPAV EAFTRGGASG PVNISTSGVY
PsaB spinach        GNFESWVQDP LHVRPIAHAI WDPHFGQPAV EAFTRGGALG PVNIAYSGVY

                    711        718        727         737        747
PsaA T.elongatus    LKVAPAI--- -QPRALSIIQ GRAVGVAHYL LGGIATTWAF FLARIISVG-
PsaA S.6803         LNVAPAI--- -QPRALSIIQ GRAVGVAHYL LGGIVTTWAF FLARSLSIG-
PsaA C.reinhardtii  LKVAPAI--- -QPRALSITQ GRAVGVAHYL LGGIATTWSF FLARIISVG-
PsaA spinach        LKVAPAT--- -QPRALSIVQ GRAVGVTHYL LGGIATTWAF FLARIIAVG-
                    691        701        711         721        731
PsaB T.elongatus    TPLANLVRWK DKPVALSIVQ ARLVGLAHFS VGYILTYAAF LIASTAAKFG
PsaB S.6803         TPLANLVRWK DKPVALSIVQ ARLVGLAHFT VGYVLTYAAF LIASTAGKFG
PsaB C.reinhardtii  TPLANLVYWK DKPVALSIVQ ARLVGLAHFS VGYIFTYAAF LIASTSGRFG
PsaB spinach        TPLANLIRWR DKPVALSIVQ ARLVGLAHFS VGYIFTYAAF LIASTSGKFG
```

FIGURE 4 Amino-acid sequences of the PsaA and PsaB subunits of PSI from *T. elongatus*, *Synechocystis* PCC 6803 (S.6803), *Chlamydomonas reinhardtii* (*C. reinhardtii*), and spinach. PsaA/PsaB residue pairs in each line were generated from the protein sequence alignment performed with the CLUSTAL program (31).

$P_A^{\bullet+}$ population, shifting the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio to 24.0:76.0 (Table 1). Thus, the influence of the accessory Chl*a* pair on the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio as well as ΔE_m appears to be significant.

For the first time to our knowledge, in this work it has been found that the difference in the energy contribution of A_{-1A}/A_{-1B} to P_A/P_B results from the orientation of the methyl-ester groups of A_{-1A}/A_{-1B}, which are orientated at an angle of ~180° to each other across the $C13^2$-$C13^3$ axis (Fig. 5). Because the methyl-ester groups are situated on the same side of the chlorin plane, the A_{-1A}/A_{-1B} pair consist of methyl-ester rotamers and not methyl-ester epimers. The carbonyl O atom of A_{-1A} is 5.4 Å away from the Mg atom of P_A whereas the corresponding distance is 7.1 Å between A_{-1B} and P_B (Fig. 5). Because the carbonyl O atom is polarized more than the ester O atom, the methyl-ester group of A_{-1A} can stabilize the cationic $P_A^{\bullet+}$ state more effectively than that of the A_{-1B} for the $P_B^{\bullet+}$ state, thus decreasing $E_m(P_A)$ relative to $E_m(P_B)$. The possible role of the methyl-ester orientation of a Chl*a* in altering the E_m of another Chl*a* in the neighborhood was originally reported in PSII (32), and our results indicate that the same phenomenon holds true for P_A/P_B in PSI. Note that a clear discrimination between the –O–CH_3 and O edges of the ester-group in the electron density map was possible at a resolution of ~2.5 Å (W. Saenger, Free University of Berlin, personal communication, 2011).

TABLE 7 PsaA/PsaB residue pairs responsible for ΔE_m (= $E_m(P_A) - E_m(P_B)$, see Fig. 2) (in mV)

PsaA			PsaB			
Residue	$E_m(P_A)$	$E_m(P_B)$	Residue	$E_m(P_A)$	$E_m(P_B)$	ΔE_m
ΔE_m decreasing pairs (i.e., pairs that contribute to accumulation of $P_A^{\bullet+}$)						
A_{-1A}	−65	−23	A_{-1B}	−19	−41	−28
Gln-A657	−4	−2	Asn-B633	18	26	−14

Contribution to ΔE_m was obtained as [influence of PsaA on $E_m(P_A)$] + [influence of PsaB on $E_m(P_A)$] – [influence of PsaA on $E_m(P_B)$] – [influence of PsaB on $E_m(P_B)$]. PsaA/PsaB residue pairs in each line were generated from the protein sequence alignment performed with the CLUSTAL program (31) (Fig. 4).

The H-bonding partner for any group that specifies the orientation of the methyl-ester groups of A_{-1A}/A_{-1B} or cause steric hindrance is absent. By rotating each methyl-ester group in A_{-1A}/A_{-1B} that is itself rotated by 180° along the $C13^2$–$C13^3$ axis, the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio changed from 27.9:72.1 (wild-type) to 22.4:77.6 (rotated methyl-ester: A_{-1A}/A_{-1B}, Table 8) and the corresponding spin-density distributions in P_A/P_B were shifted from 22.4:77.6 to 15.1:84.9, respectively. The spin-density distribution of 15.1:84.9 was considerably shifted from the wild-type PSI value. A similar value of the spin-density distribution (15:85) was reported from EPR studies of PSI from *T. elongatus* (8). As the energy required for rotation of the methyl-ester group is not unusually large (due to the sp^3 carbons) and the H-bonding partner that specifies the orientation of the methyl-ester groups of A_{-1A}/A_{-1B} is absent, it is reasonable to assume that the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio and the

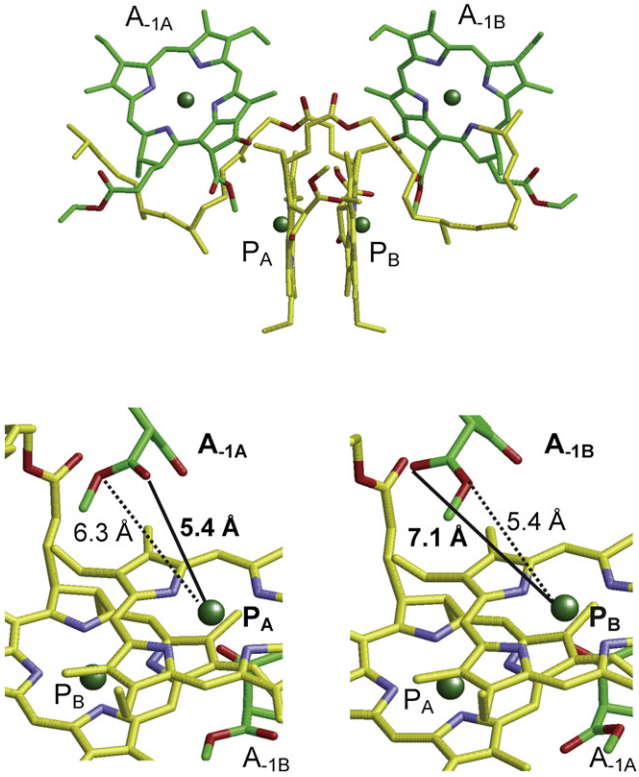

FIGURE 5 Geometry of the accessory Chl*a* A_{-1A} and A_{-1B}. (*Solid* and *dotted lines*) Distances between the Mg atom and the O atoms of the carbonyl and ester groups, respectively.

spin-density distribution over P_A/P_B fluctuates within the ranges given in Table 8. Hence, the orientation of the methyl-ester group in A_{-1A}/A_{-1B} can affect the P_A/P_B ΔE_m and the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio.

CONCLUSIONS

The $P_A^{\bullet+}/P_B^{\bullet+}$ ratio of the P_A/P_B dimer calculated over the entire PSI protein was 28:72, which was close to the charge-distribution ratio of 33:67 obtained in the FTIR studies of PSI from *Synechocystis* sp. PCC 6803 (6). The calculated spin density, which was asymmetrically distributed over the P_A/P_B dimer with a ratio of 22:78, was in good agreement with the experimental values of 25:75 (4) and 20:80 in EPR studies from spinach (7). The Chl*a*′/Chl*a* difference for P_A/P_B was revealed to be partially responsible for the larger population of the $P_B^{\bullet+}$ state, from the methyl-ester deletion simulations. Removal of the H-bond between P_A and Thr-A743 in T(A743)V mutation resulted in a slight decrease in $E_m(P_A)$ and a partial movement of the cationic state from P_A to P_B, as suggested by mutational studies (27,28).

Conserved PsaA/PsaB pairs, Arg-A651/Arg-B627 and Arg-A728/Arg-B712 upshifted both $E_m(P_A)$ and $E_m(P_B)$ by ~30 mV, and Asp-A463/Asp-B444 and Asp-A593/Asp-B580 residue pairs downshifted both $E_m(P_A)$ and $E_m(P_B)$ in the range ~30–60 mV. The residue pair that led to a notable value of ΔE_m (i.e., $E_m(P_A) > E_m(P_B)$) was Arg-A750/Ser-B734, with a ΔE_m of 17 mV, thus contributing to an increase in the $P_B^{\bullet+}$ population (Note that a simple mutation of the residues would cause a change in the protonation states of the titratable residues in PSI, compensating for changes in the net charges of the mutated sites.). On the other hand, the most influential pair enhancing $E_m(P_A) < E_m(P_B)$ was the accessory A_{-1A}/A_{-1B} Chl*a* pair, with a ΔE_m of 28 mV; this pair contributed to an increase in the $P_A^{\bullet+}$ population in the original PSI crystal structure. The different influence of A_{-1A} and A_{-1B} on $E_m(P_A)$ and $E_m(P_B)$ was due to the differences in their methyl-ester orientations. Rotation of the methyl-ester groups alters the P_A/P_B spin-density distributions from 22:78 to 15:85. The latter value was in agreement with the value of 15:85 measured by EPR for PSI from *T. elongatus* (8).

TABLE 8 Influence of the orientation of the methyl-ester group of A_{-1A}/A_{-1B} on the $P_A^{\bullet+}/P_B^{\bullet+}$ ratio and spin-density distribution calculated in the PSI protein (in %)

	Charge		Spin	
	$P_A^{\bullet+}$	$P_B^{\bullet+}$	P_A	P_B
Wild-type	27.9	72.1	22.4	77.6
	[Rotated methyl-ester]			
A_{-1A}	26.6	73.4	19.7	80.3
A_{-1B}	23.5	76.5	17.4	82.6
A_{-1A}/A_{-1B}	22.4	77.6	15.1	84.9

SUPPORTING MATERIAL

One table is available at http://www.biophysj.org/biophysj/supplemental/S0006-3495(11)01064-2.

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